

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	501.5	82.2	450	6	US-10-542-508-45	Sequence 45, Appl
2	501.5	82.2	450	6	US-10-542-508-51	Sequence 51, Appl
3	500	82.0	125	7	US-11-095-822-58	Sequence 58, Appl
4	500	82.0	125	7	US-11-096-074-58	Sequence 58, Appl
5	497.5	81.6	122	6	US-10-413-703B-13	Sequence 13, Appl
6	497.5	81.6	450	6	US-10-542-508-47	Sequence 47, Appl
7	497.5	81.6	450	6	US-10-542-508-53	Sequence 53, Appl
8	497.5	81.6	467	6	US-10-543-508-68	Sequence 68, Appl
9	497	81.5	117	5	US-09-490-064-22	Sequence 22, Appl
10	497	81.5	123	7	US-11-039-767-14	Sequence 14, Appl
11	494.5	81.1	245	7	US-11-054-515-1919	Sequence 1919, Ap
12	494	81.0	129	6	US-10-965-616-77	Sequence 77, Appl
13	492.5	80.7	245	7	US-11-054-515-1902	Sequence 1902, Ap
14	491.5	80.6	120	5	US-09-490-064-36	Sequence 36, Appl
15	491.5	80.6	120	5	US-09-490-064-59	Sequence 59, Appl
16	490.5	80.4	255	7	US-11-054-515-1156	Sequence 1156, Ap
17	490.5	80.4	450	6	US-10-542-508-49	Sequence 49, Appl
18	489.5	80.2	116	8	US-60-674-082-98	Sequence 98, Appl
19	489	80.2	142	7	US-11-158-505-36	Sequence 36, Appl
20	488.5	80.1	249	7	US-11-054-515-1290	Sequence 1290, Ap
21	488.5	80.1	249	7	US-11-054-515-1299	Sequence 1299, Ap
22	488.5	80.1	254	7	US-11-054-515-1983	Sequence 1983, Ap
23	488.5	80.1	448	7	US-11-158-505-8	Sequence 8, Appl
24	488.5	80.1	448	7	US-11-158-505-16	Sequence 16, Appl
25	488.5	80.1	448	7	US-11-158-505-24	Sequence 24, Appl

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OM protein - protein search, using sw model

Run on: August 27, 2005, 01:50:17 ; Search time 161 Seconds

(without alignments)
280.662 Million cell updates/sec

Title: US-09-856-114A-21

Perfect score: 610
Sequence: 1 QVQLVQSGAEVKKPGASVKV.....CAREYDEAYWGQGLTVTVSS 115

Scoring table: BLASTUM62

Gapop 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	540	88.5	119	18	US-10-981-738-48
2	536	87.9	119	18	US-10-981-738-30
3	531	87.0	119	18	US-10-981-738-44
4	529	86.7	119	18	US-10-981-738-54
5	527	86.4	119	18	US-10-981-738-46
6	522.5	85.7	139	10	US-09-269-921-110
7	522.5	85.7	139	10	US-09-509-098-20
8	522.5	85.7	139	14	US-10-218-253-110
9	519.5	85.2	139	10	US-09-269-921-111
10	519.5	85.2	139	10	US-09-509-098-22
11	519.5	85.2	139	14	US-10-218-253-111

12	519	85.1	119	18	US-10-981-738-32
13	518.5	85.0	139	9	US-09-760-723-7
14	518.5	85.0	139	9	US-09-355-925-8
15	518.5	85.0	139	10	US-09-269-921-125
16	518.5	85.0	139	10	US-09-509-098-50
17	518.5	85.0	139	14	US-10-315-125-7
18	518.5	85.0	139	14	US-10-218-253-125
19	518.5	85.0	139	14	US-10-428-085-7
20	518	84.9	119	18	US-10-981-738-36
21	516.5	84.7	139	10	US-09-269-921-108
22	516.5	84.7	139	10	US-09-509-098-16
23	516.5	84.7	139	14	US-10-218-253-108
24	515	84.4	119	18	US-10-981-738-40
25	514.5	84.3	139	9	US-09-760-723-8
26	514.5	84.3	139	9	US-09-355-925-8
27	514.5	84.3	139	10	US-09-269-921-128
28	514.5	84.3	139	10	US-09-509-098-127
29	514.5	84.3	139	14	US-10-315-125-8
30	514.5	84.3	139	14	US-10-218-253-128
31	514.5	84.3	139	14	US-10-428-085-8
32	514.5	84.3	139	16	US-10-474-714-6
33	514	84.3	119	18	US-10-981-738-38
34	513.5	84.2	139	10	US-09-269-921-109
35	513.5	84.2	139	10	US-09-509-098-18
36	513.5	84.2	139	14	US-10-218-253-109
37	512.5	84.0	139	10	US-09-269-921-123
38	512.5	84.0	139	10	US-09-269-921-124
39	512.5	84.0	139	10	US-09-509-098-46
40	512.5	84.0	139	10	US-09-509-098-48
41	512.5	84.0	139	14	US-10-218-253-123
42	512.5	84.0	139	14	US-10-218-253-124
43	511.5	83.9	139	10	US-09-269-921-114
44	511.5	83.9	139	10	US-09-509-098-28
45	511.5	83.9	139	14	US-10-218-253-114

ALIGNMENTS

RESULT 1
US-10-981-738-48
; Sequence 48, Application US/10981738
; Publication No. US20050123546A1
; GENERAL INFORMATION:
; APPLICANT: Umana, Pablo
; APPLICANT: Bruenker, Peter
; APPLICANT: Suter, Tobias
; APPLICANT: Puenteener, Ursula
; APPLICANT: Moesner, Ekkehard
; APPLICANT: Ferrara, Claudia
; TITLE OF INVENTION: Antigen Binding Molecules with Increased Fc Receptor Binding
; TITLE OF INVENTION: Affinity and Effector Function
; FILE REFERENCE: 1975.0290001
; CURRENT APPLICATION NUMBER: US/10/981,738
; CURRENT FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Mouse-human chimeric polypeptide
US-10-981-738-48

Query Match 88.5%; Score 540; DB 18; Length 119;
Best Local Similarity 88.2%; Pred. No. 8.3e-40;
Matches 105; Conservative 3; Mismatches 7; Indels 4; Gaps 1;
QY 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSSMMWVRQAPGQGLEWMGRITPGDGTNY 60
DB 1 QVQLVQSGAEVKKPGASVKVCKASGYTFTSSMMWVRQAPGQGLEWMGRITPGDGTNY 60

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OM protein - protein search, using sw model

Run on: August 27, 2005, 01:33:46 ; Search time 43 Seconds
(without alignments)
199.643 Million cell updates/sec

Title: US-09-856-114a-21
Perfect score: 610
Sequence: 1 QVLQSGAEVKPKASVKV.....CAREYDEAYWGQGLTVTVSS 115

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:
6: /cgn2_6/prodata/1/1aa/backfillresi.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	522.5	85.7	139	4	US-09-269-921-110 Sequence 110, App
2	519.5	85.2	139	4	US-09-269-921-111 Sequence 111, App
3	518.5	85.0	139	4	US-09-355-925-7 Sequence 7, Appl
4	518.5	85.0	139	4	US-09-269-921-125 Sequence 125, App
5	516.5	84.7	139	4	US-09-269-921-108 Sequence 108, App
6	514.5	84.3	139	4	US-09-355-925-8 Sequence 8, Appl
7	514.5	84.3	139	4	US-09-269-921-128 Sequence 128, App
8	513.5	84.2	139	4	US-09-269-921-109 Sequence 109, App
9	512.5	84.0	139	4	US-09-269-921-123 Sequence 123, App
10	512.5	84.0	139	4	US-09-269-921-124 Sequence 124, App
11	511.5	83.9	139	4	US-09-269-921-114 Sequence 114, App
12	509.5	83.5	139	4	US-09-269-921-112 Sequence 112, App
13	507	83.1	119	4	US-09-438-954-4 Sequence 4, Appl
14	505.5	82.9	139	4	US-09-269-921-115 Sequence 115, App
15	502.5	82.4	139	4	US-09-269-921-118 Sequence 118, App
16	501.5	82.2	139	4	US-09-269-921-113 Sequence 113, App
17	501.5	82.2	139	4	US-09-269-921-122 Sequence 122, App
18	499.5	81.9	139	4	US-09-269-921-121 Sequence 121, App
19	498.5	81.7	139	4	US-09-269-921-117 Sequence 117, App
20	497	81.5	117	3	US-09-025-769B-22 Sequence 22, Appl
21	497	81.5	117	4	US-09-490-070A-22 Sequence 22, Appl
22	497	81.5	117	4	US-09-490-153-22 Sequence 22, Appl
23	497	81.5	117	4	US-09-490-324-22 Sequence 22, Appl
24	496.5	81.4	139	4	US-09-269-921-119 Sequence 119, App
25	494	81.0	129	2	US-08-561-521-45 Sequence 45, Appl
26	494	81.0	129	3	US-08-525-539A-77 Sequence 77, Appl
27	494	81.0	129	5	PCT-US95-01219-45 Sequence 45, Appl

28	493.5	80.9	139	4	US-09-269-921-116 Sequence 116, App
29	492.5	80.7	139	4	US-09-269-921-120 Sequence 120, App
30	491.5	80.6	120	3	US-09-025-769B-36 Sequence 36, Appl
31	491.5	80.6	120	3	US-09-025-769B-59 Sequence 59, Appl
32	491.5	80.6	120	4	US-09-490-070A-36 Sequence 36, Appl
33	491.5	80.6	120	4	US-09-490-070A-59 Sequence 59, Appl
34	491.5	80.6	120	4	US-09-490-153-36 Sequence 36, Appl
35	491.5	80.6	120	4	US-09-490-153-59 Sequence 59, Appl
36	491.5	80.6	120	4	US-09-490-324-36 Sequence 36, Appl
37	491.5	80.6	120	4	US-09-490-324-59 Sequence 59, Appl
38	488.5	80.1	128	1	US-08-202-047-22 Sequence 22, Appl
39	488.5	80.1	128	3	US-08-964-690-22 Sequence 22, Appl
40	486	79.7	123	1	US-08-477-877B-94 Sequence 94, Appl
41	486	79.7	123	2	US-08-472-281A-94 Sequence 94, Appl
42	486	79.7	123	2	US-08-477-989B-94 Sequence 94, Appl
43	484	79.3	119	4	US-09-254-180C-18 Sequence 18, Appl
44	483.5	79.3	139	4	US-09-269-921-126 Sequence 126, App
45	481.5	78.9	118	3	US-08-513-968-80 Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-09-269-921-110
; Sequence 110, Application US/09269921
; Patent No. 6699974
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/09/269,921
; EARLIER FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: PCT/JP97/03553
; EARLIER FILING DATE: 1997-10-03
; EARLIER APPLICATION NUMBER: JP 8-264756
; EARLIER FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 110
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; OTHER INFORMATION: of reshaped human anti-HM 1.24 antibody H chain V region
; OTHER INFORMATION: version C
US-09-269-921-110

Query Match 85.7%; Score 522.5; DB 4; Length 139;
Best Local Similarity 85.0%; Pred. No. 5.5e-44;
Matches 102; Conservative 3; Mismatches 10; Indels 5; Gaps 1;

QY 1 QVLQSGAEVKPKASVKVCKASGYTPTSSWMNVROAPQGLWMGRVPGDGTNY 60
Db 20 QVLQSGAEVKPKASVKVCKASGYTPTSSWMNVROAPQGLWMGRVPGDGTNY 79
QY 61 AQKFGQRYTMTADKSTSTVTYMLSLRSEDVAVYTCAR-----EYDEAYWGQGLTVTVSS 115
Db 80 SQKFGQRYTMTADKSTSTVTYMLSLRSEDVAVYTCARGLRRGGYFYDWGQGLTVTVSS 139

RESULT 2
US-09-269-921-111
; Sequence 111, Application US/09269921
; Patent No. 6699974
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko

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OM protein - protein search, using sw model

Run on: August 27, 2005, 00:50:05 ; Search time 174 Seconds
(without alignments)
338.443 Million cell updates/sec

Title: US-09-856-114a-21
Perfect score: 610
Sequence: 1 QVQLVQSGAEYVKPGASVKV.....CAREYDRAYWGQGLVTVSS 115

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.:

1: uniprot_sprot.:

2: uniprot_trembl.:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483.5	79.3	124	2	Q9UL92
2	480	78.7	614	2	Q7TMT6
3	463.5	76.0	498	2	Q6N041
4	457	74.9	244	2	Q65ZC8
5	456.5	74.8	159	2	Q9Q080
6	452	74.1	119	2	Q9UL94
7	451	73.9	119	2	Q9GYZ2
8	445.1	73.9	125	2	Q9UL95
9	444.5	72.9	118	2	Q921C4
10	444.5	72.9	518	2	Q6N030
11	441	72.3	117	1	HV1B HUMAN
12	441	72.3	473	2	Q9DBL4
13	438	71.8	464	2	Q6PF95
14	437.5	71.7	116	2	Q9UL89
15	431	70.7	142	2	Q924O1
16	430	70.5	140	2	Q924R2
17	430	70.5	500	2	Q6N091
18	427	70.0	117	1	HV1G HUMAN
19	426.5	69.9	139	2	Q924R5
20	426.5	69.9	143	2	Q924P9
21	426.5	69.9	143	2	Q924Q0
22	426.5	69.9	145	2	Q924R4
23	426	69.8	140	2	Q924P8
24	424	69.5	474	2	Q8R3H6
25	423.5	69.4	141	2	Q924Q4
26	423.5	69.4	143	2	Q924R0
27	422.5	69.3	143	2	Q924Q5
28	422.5	69.3	147	1	HV1C HUMAN
29	422.5	69.3	482	2	Q8K172
30	422	69.2	146	2	Q924Q3
31	422	69.2	481	2	Q91WT1

ALIGNMENTS

RESULT 1

Q9UL92 PRELIMINARY; PRT; 124 AA.

AC Q9UL92; 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAY-2000 (Tremblrel. 25, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable region

DE (Fragment).

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

EX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035022; AAD56258.1; -

DR HSP; P01751; INOB.

DR InterPro; IPR007110; Ig-like.

DR SMART; IPR003596; IG_V.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PSS0835; IG_LIKE; 1.

FT NON_TER 1_124

FT NON_TER 124 124

SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 79.3%; Score 483.5; DB 2; Length 124;

Best Local Similarity 77.0%; Pred. No. 1.9e-42;

Matches 97; Conservative 7; Mismatches 9; Indels 13; Gaps 2;

QY 1 QVQLVQSGAEYVKPGASVKVSKASGYTFTSGMMVVRQAPQGLFWMGRIYPGDGTNY 60

Db 1 EVQLVESGAEVKPGASVKVSKASGYTFTSSYMHVVRQAPQGLFWMGRIYPGDGTNY 60

QY 61 AQKQGRVTMTADKSTSTVYMLSLRSEDYAVYCAR-----EYDEAYWGQGT 109

Db 61 AQKQGRVTMTADKSTSTVYMLSLRSEDYAVYCARGLYVVPAAFRFPD--YWGQGT 118

QY 110 LVTSS 115

Db 119 LVTSS 124

RESULT 2

ID Q7TMT6 PRELIMINARY; PRT; 614 AA.

AC Q7TMT6; 25, Created)

DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)

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OM protein - protein search, using sw model

Run on: August 27, 2005, 01:29:01 ; Search time 39 Seconds
(without alignments)
283.716 Million cell updates/sec

Title: US-09-856-114A-21
Perfect score: 610
Sequence: 1 QVQLVQSGAEVKKPGASVK
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	489	80.2	142	2 A32483	Ig heavy chain V r
2	488.5	80.1	118	2 S36265	Ig heavy chain V r
3	478.5	78.4	135	2 S49530	anti-Sm antibody V
4	471.5	77.3	119	2 A24672	Ig heavy chain pre
5	468	76.7	121	2 S20783	Ig heavy chain V r
6	465	76.2	123	2 D33548	Ig heavy chain V-1
7	464	76.1	129	2 A33548	Ig heavy chain V-1
8	463.5	76.0	120	2 PH0962	Ig heavy chain V r
9	460	75.4	119	2 PH0961	Ig heavy chain V r
10	459.5	75.3	128	2 PH0952	Ig heavy chain V r
11	458	75.1	129	2 S46393	Ig heavy chain V r
12	457	74.9	125	2 PH0957	Ig heavy chain V r
13	456.5	74.8	136	2 S31600	Ig heavy chain V r
14	455.5	74.7	116	2 PH0959	Ig heavy chain V r
15	455	74.6	122	2 S36271	Ig heavy chain V r
16	454	74.4	118	2 PL0231	Ig heavy chain V r
17	451.5	74.0	136	2 PH0960	Ig heavy chain V r
18	450.5	73.9	122	2 PH0958	Ig heavy chain V r
19	449.5	73.7	120	2 B22769	Ig heavy chain V r
20	449.5	73.7	140	2 S03216	Ig heavy chain pre
21	449	73.6	160	2 PL0105	anti-PR2 erythrocy
22	448.5	73.5	132	2 PH0954	Ig heavy chain V r
23	446	73.1	98	2 S25920	Ig heavy chain V r
24	445.5	73.0	124	2 S19665	Ig heavy chain V r
25	445	73.0	129	2 S36260	Ig heavy chain V r
26	445	73.0	133	2 C33548	Ig heavy chain V-1
27	445	73.0	627	2 S14683	Ig mu chain precu
28	444	72.8	127	2 PH0955	Ig heavy chain V r
29	443	72.6	113	2 PH1428	Ig heavy chain V r

30	443	72.6	119	2 D30562	Ig heavy chain V r
31	443	72.6	126	2 I44151	Ig heavy chain V r
32	443	72.6	135	2 PH0953	Ig heavy chain V r
33	442.5	72.5	117	2 PL0237	Ig heavy chain V r
34	442.5	72.5	132	2 S46394	Ig heavy chain V r
35	442.5	72.5	139	2 PH1558	Ig heavy chain V r
36	442.5	72.5	171	2 S23623	Ig heavy chain V r
37	442	72.5	112	2 PL0232	Ig heavy chain V r
38	441.5	72.4	116	2 S09962	Ig heavy chain V-D
39	441.5	72.4	117	2 PL0235	Ig heavy chain V r
40	441.5	72.4	126	2 B33548	Ig heavy chain V-1
41	441	72.3	117	1 HVHUG	Ig heavy chain pre
42	440.5	72.2	104	2 PH1665	Ig heavy chain V r
43	440	72.1	119	2 C30562	Ig heavy chain V r
44	439.5	72.0	115	2 PL0238	Ig heavy chain V r
45	438.5	71.9	110	2 PH1669	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A32483
Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C:Accession: A32483
R:Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A>Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells us
A:Reference number: A32483; MUID:89273586; PMID:2499327
A:Accession: A32483
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-142 <LAR>

A:Cross-references: GB:M26463
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:25-108/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 489; DB 2; Length 142;
Best Local Similarity 78.0%; Pred. No. 3.6e-37;
Matches 99; Conservative 3; Mismatches 13; Indels 12; Gaps 1;

QY	1	QVQLVQSGAEVKKPGASVKASVKTFTSSMMNVRQAPGQGLEWMGRIYPCGDGTNY	60
DB	11	QVQLVQSGAEVKKPGASVKASVKTFTTNYMHVRQAPGQGLEWMGIINSGNSTNY	70
QY	61	AQKPGQGRVTMTADKSTSTVYMELSLRSDTAVTYCARE-----YDEAYWGQ	108
DB	71	AQKPGQGRVTMTADKSTSTVYMELSLRSDTAVTYCAREKLATTIFGVLIITGMDYWGQ	130
QY	109	TLVTSS	115
DB	131	TLVTSS	137

RESULT 2

S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36265
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993
A>Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36265; MUID:93178448; PMID:7679990
A:Accession: S36265
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-118 <GRI>

A:Cross-references: EMBL:Z18846; NID:g33121; PIDN:CAA79298.1; PID:g939900
C:Superfamily: immunoglobulin V region; immunoglobulin homology

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: August 27, 2005, 01:44:36 ; Search time 486 Seconds
(without alignments)
276.380 Million cell updates/sec

Title: US-09-856-114A-21
Perfect score: 610
Sequence: 1 QVQLVQSGAEVKKPQASVKV.....CAREYDEAYWGQGLVTVSS 115

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_Main*

- 1: /cgm2_6/ptodata/1/paa/PCTUS_COMB.pep.*
- 2: /cgm2_6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgm2_6/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgm2_6/ptodata/1/paa/US080_COMB.pep.*
- 5: /cgm2_6/ptodata/1/paa/US081_COMB.pep.*
- 6: /cgm2_6/ptodata/1/paa/US082_COMB.pep.*
- 7: /cgm2_6/ptodata/1/paa/US083_COMB.pep.*
- 8: /cgm2_6/ptodata/1/paa/US084_COMB.pep.*
- 9: /cgm2_6/ptodata/1/paa/US085_COMB.pep.*
- 10: /cgm2_6/ptodata/1/paa/US086_COMB.pep.*
- 11: /cgm2_6/ptodata/1/paa/US087_COMB.pep.*
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- 25: /cgm2_6/ptodata/1/paa/US099B_COMB.pep.*
- 26: /cgm2_6/ptodata/1/paa/US100_COMB.pep.*
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- 29: /cgm2_6/ptodata/1/paa/US103_COMB.pep.*
- 30: /cgm2_6/ptodata/1/paa/US104_COMB.pep.*
- 31: /cgm2_6/ptodata/1/paa/US105_COMB.pep.*
- 32: /cgm2_6/ptodata/1/paa/US106_COMB.pep.*
- 33: /cgm2_6/ptodata/1/paa/US107_COMB.pep.*
- 34: /cgm2_6/ptodata/1/paa/US108_COMB.pep.*
- 35: /cgm2_6/ptodata/1/paa/US109_COMB.pep.*
- 36: /cgm2_6/ptodata/1/paa/US110_COMB.pep.*
- 37: /cgm2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	610	100.0	115	18	US-09-485-071A-21	Sequence 21, Appl
2	610	100.0	115	23	US-09-856-114-21	Sequence 21, Appl
3	610	100.0	115	23	US-09-856-114A-21	Sequence 21, Appl
4	592	97.0	115	18	US-09-485-071A-33	Sequence 33, Appl
5	572	93.8	115	18	US-09-485-071A-20	Sequence 20, Appl
6	572	93.8	115	23	US-09-856-114-20	Sequence 20, Appl
7	572	93.8	115	23	US-09-856-114A-20	Sequence 20, Appl
8	540	88.5	119	35	US-10-981-738-48	Sequence 48, Appl
9	536	87.9	119	35	US-10-981-738-30	Sequence 30, Appl
10	531	87.0	119	35	US-10-981-738-44	Sequence 44, Appl
11	529	86.7	119	35	US-10-981-738-54	Sequence 54, Appl
12	527	86.4	119	35	US-10-981-738-46	Sequence 46, Appl
13	522.5	85.7	139	19	US-09-509-098-20	Sequence 20, Appl
14	522.5	85.7	139	28	US-10-218-253-110	Sequence 110, Appl
15	519.5	85.2	139	19	US-09-509-098-22	Sequence 22, Appl
16	519.5	85.2	139	28	US-10-218-253-111	Sequence 111, Appl
17	519	85.1	139	35	US-10-981-738-32	Sequence 32, Appl
18	518.5	85.0	139	17	US-09-367-833B-7	Sequence 7, Appl
19	518.5	85.0	139	19	US-09-509-098-50	Sequence 50, Appl
20	518.5	85.0	139	19	US-09-509-5308-7	Sequence 7, Appl
21	518.5	85.0	139	20	US-09-622-646-28	Sequence 28, Appl
22	518.5	85.0	139	22	US-09-760-723-7	Sequence 7, Appl
23	518.5	85.0	139	28	US-10-218-253-125	Sequence 125, Appl
24	518.5	85.0	139	29	US-10-315-125-7	Sequence 7, Appl
25	518.5	85.0	139	30	US-10-428-085-7	Sequence 7, Appl
26	518	84.9	119	35	US-10-981-738-36	Sequence 36, Appl
27	516.5	84.7	139	19	US-09-509-098-16	Sequence 16, Appl
28	516.5	84.7	139	28	US-10-218-253-108	Sequence 108, Appl
29	515	84.4	139	35	US-10-981-738-40	Sequence 40, Appl
30	514.5	84.3	139	17	US-09-367-833B-8	Sequence 8, Appl
31	514.5	84.3	139	19	US-09-509-098-127	Sequence 127, Appl
32	514.5	84.3	139	19	US-09-509-5308-8	Sequence 8, Appl
33	514.5	84.3	139	20	US-09-622-646-29	Sequence 29, Appl
34	514.5	84.3	139	22	US-09-760-723-8	Sequence 8, Appl
35	514.5	84.3	139	28	US-10-218-253-128	Sequence 128, Appl
36	514.5	84.3	139	29	US-10-315-125-8	Sequence 8, Appl
37	514.5	84.3	139	30	US-10-428-085-8	Sequence 8, Appl
38	514.5	84.3	139	30	US-10-474-714-6	Sequence 6, Appl
39	514	84.3	119	35	US-10-981-738-38	Sequence 38, Appl
40	513.5	84.2	139	19	US-09-509-098-18	Sequence 18, Appl
41	513.5	84.2	139	28	US-10-218-253-109	Sequence 109, Appl
42	512.5	84.0	139	19	US-09-509-098-46	Sequence 46, Appl
43	512.5	84.0	139	19	US-09-509-098-48	Sequence 48, Appl
44	512.5	84.0	139	28	US-10-218-253-123	Sequence 123, Appl
45	512.5	84.0	139	28	US-10-218-253-124	Sequence 124, Appl

ALIGNMENTS

RESULT 1
US-09-485-071A-21
Sequence 21, Application US/09485071A
GENERAL INFORMATION:
APPLICANT: HYO Jeong Hong
APPLICANT: Chun Jeih Ryu
TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR SURFACE
TITLE OF INVENTION: ANTIGEN PRE-S1 OF HBV AND PREPARATION METHOD THEREOF
FILE REFERENCE: 118.13USWO
CURRENT APPLICATION NUMBER: US/09/485,071A
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: PCT/KR99/00699
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 1998-49663
PRIOR FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21